

5'	9	18	27	36	45	54													
NNC	TGT	AAT	AGG	AGC	AGT	ATA	GGG	AAA	CCT	GGT	ACC	CTG	CAG	GTA	CTG	GTC	CGG		
	63	72	81	90	99	108													
AGT	TCC	TGG	GTC	GAC	CCA	CGC	GTC	CGG	CTT	TCT	GTA	GCT	GTA	ACA	TTG	GTG	GCC		
	117	126	135	144	153	162													
ACA	CAC	CTC	CTT	ACA	AAG	CAA	CTA	GAA	CCT	GCG	GCA	TAC	ATT	GGA	GAG	ATT	TTT		
	171	180	189	198	207	216													
TTA	ATT	TTC	TGG	ACA	TGA	AGT	AAA	TTT	AGA	GTG	CTT	TCT	AAT	TTC	AGG	TAG	AAG		
	225	234	243	252	261	270													
ACA	TGT	CCA	CCT	TCT	GAT	TAT	TTT	TGG	AGA	ACA	TTT	TGA	TTT	TTT	TCA	TCT	CTC		
	279	288	297	306	315	324													
TCT	CCC	CAC	CCC	TAA	GAT	TGT	GCA	AAA	AAA	GCG	TAC	CTT	GCC	TAA	TTG	AAA	TAA		
	333	342	351	360	369	378													
TTT	CAT	TGG	ATT	TTG	ATC	AGA	ACT	GAT	TAT	TTG	GTT	TTC	TGT	GTG	AAG	TTT	TGA		
	387	396	405	414	423	432													
GGT	TTC	AAA	CTT	TCC	TTC	TGG	AGA	ATG	CCT	TTT	GAA	ACA	ATT	TTC	TCT	AGC	TGC		
	441	450	459	468	477	486													
CTG	ATG	TCA	ACT	GCT	TAG	TAA	TCA	GTG	GAT	ATT	GAA	ATA	TTC	AAA	ATG	TAC	AGA		
															M	Y	R		
	495	504	513	522	531	540													
GAG	TGG	GTA	GTG	GTG	AAT	GTT	TTC	ATG	ATG	TTG	TAC	GTC	CAG	CTG	GTG	CAG	GGC		
E	W	V	V	V	N	V	F	M	M	L	Y	V	Q	L	V	Q	G		
	549	558	567	576	585	594													
TCC	AGT	AAT	GAA	CAT	GGA	CCA	GTG	AAG	CGA	TCA	TCT	CAG	TCC	ACA	TTG	GAA	CGA		
S	S	N	E	H	G	P	V	K	R	S	S	Q	S	T	L	E	R		
	603	612	621	630	639	648													
TCT	GAA	CAG	CAG	ATC	AGG	GCT	GCT	TCT	AGT	TTG	GAG	GAA	CTA	CTT	CGA	ATT	ACT		
S	E	Q	Q	I	R	A	A	S	S	L	E	E	L	L	R	I	T		
	657	666	675	684	693	702													
CAC	TCT	GAG	GAC	TGG	AAG	CTG	TGG	AGA	TGC	AGG	CTG	AGG	CTC	AAA	AGT	TTT	ACC		
H	S	E	D	W	K	L	W	R	C	R	L	R	L	K	S	F	T		
	711	720	729	738	747	756													
AGT	ATG	GAC	TCT	CGC	TCA	GCA	TCC	CAT	CGG	TCC	ACT	AGG	TTT	GCG	GCA	ACT	TTC		
S	M	D	S	R	S	A	S	H	R	S	T	R	F	A	A	T	F		
	765	774	783	792	801	810													
TAT	GAC	ATT	GAA	ACA	CTA	AAA	GTT	ATA	GAT	GAA	GAA	TGG	CAA	AGA	ACT	CAG	TGC		
Y	D	I	E	T	L	K	V	I	D	E	E	W	Q	R	T	Q	C		

FIGURE 1A

819	828	837	846	855	864
AGC CCT AGA GAA ACG TGC GTG GAG GTG GCC AGT GAG CTG GGG AAG AGT ACC AAC					
S P R E T C V E V A S E L G K S T N					
873	882	891	900	909	918
ACA TTC TTC AAG CCC CCT TGT GTG AAC GTG TTC CGA TGT GGT GGC TGT TGC AAT					
T F F K P P C V N V F R C G G C C N					
927	936	945	954	963	972
GAA GAG AGC CTT ATC TGT ATG AAC ACC AGC ACC TCG TAC ATT TCC AAA CAG CTC					
E E S L I C M N T S T S Y I S K Q L					
981	990	999	1008	1017	1026
TTT GAG ATA TCA GTG CCT TTG ACA TCA GTA CCT GAA TTA GTG CCT GTT AAA GTT					
F E I S V P L T S V P E L V P V K V					
1035	1044	1053	1062	1071	1080
GCC AAT CAT ACA GGT TGT AAG TGC TTG CCA ACA GCC CCC CGC CAT CCA TAC TCA					
A N H T G C K C L P T A P R H P Y S					
1089	1098	1107	1116	1125	1134
ATT ATC AGA AGA TCC ATC CAG ATC CCT GAA GAA GAT CGC TGT TCC CAT TCC AAG					
I I R R S I Q I P E E D R C S H S K					
1143	1152	1161	1170	1179	1188
AAA CTC TGT CCT ATT GAC ATG CTA TGG GAT AGC AAC AAA TGT AAA TGT GTT TTG					
K L C P I D M L W D S N K C K C V L					
1197	1206	1215	1224	1233	1242
CAG GAG GAA AAT CCA CTT GCT GGA ACA GAA GAC CAC TCT CAT CTC CAG GAA CCA					
Q E E N P L A G T E D H S H L Q E P					
1251	1260	1269	1278	1287	1296
GCT CTC TGT GGG CCA CAC ATG ATG TTT GAC GAA GAT CGT TGC GAG TGT GTC TGT					
A L C G P H M M F D E D R C E C V C					
1305	1314	1323	1332		
AAA ACA CCA TGT CCC AAG ATC TAA TCC AGC ACC CCA AAA AAT G 3'					
K T P C P K I * S S T P K N					

FIGURE 1B

1 MYREWVVVNVM ---MLYVQLVQGSSNEHGPVKRSSQST 873352  
1 MH ---LLGFFSVACSLLAALLPGLPGPREAPAAA - AFESG GI 1150989

37 LERS --- ---EQQIRAAASSLEELLRITHS 873352  
36 LDLSDAEPDAGEATAYASKDLEQLRSLVSSVDELMTVLYP GI 1150989

60 EDWKLWRCRLRLKSE --- ---TSMDSRSASHRSTRFAATF 873352  
76 EYWKMYKCLRLKGGWQHNRREQANLSR - -TEETIKFAAAH GI 1150989

94 YDIETLKVIDEEWQRTQCSPRETCVEVASELGKSTNTFFK 873352  
114 YNTEILKSIDNEWRKTQCMPREVCLIDVKGELFVATNTFFK GI 1150989

134 PPCVNVFRCGGCCNEESLICMNTSTSYISKQLFEISVPLT 873352  
154 PPCVSIVYRCGGCCNSEGLQCMNTSTSYLSKTLFEITVPLS GI 1150989

174 SVPELVVPVKVANHTGCKCLPTAP - -RHYPYSIIRRSIQIPE 873352  
194 QGPKPVTISFANHSTSCRCMSKLDVYRQVHSHIIRRS LP - AT GI 1150989

212 EDRCSHKKLCPI DMLWDSNKKCKVLQEEENPLAGTED - - 873352  
233 LPQCQAANKTCPTNYMWNHNI CRCLAQEEDFMFSSDAGDDS GI 1150989

249 --- ---HSHLOE --- --- --- 873352  
273 TDGFHDICGPNKELDEETCQCVCRAGLRPA SCGPHKELDR GI 1150989

255 --- ---PALCGPHMMFDEDRCECVCKTPCPK - - 873352  
313 NSCQCVCCKNKLFFSQCGGANREFDENTCQCVCKRTCPRNQP GI 1150989

280 --- --- --- --- --- --- 873352  
353 LNPCKACECTESPQCKLLKGKFFHHQTCS CYRRPCTNRQ GI 1150989

280 --- --- --- --- --- ---I 873352  
393 KACEPGFSYSEEVCRCPSPSYWKRFQMS GI 1150989

FIGURE 2

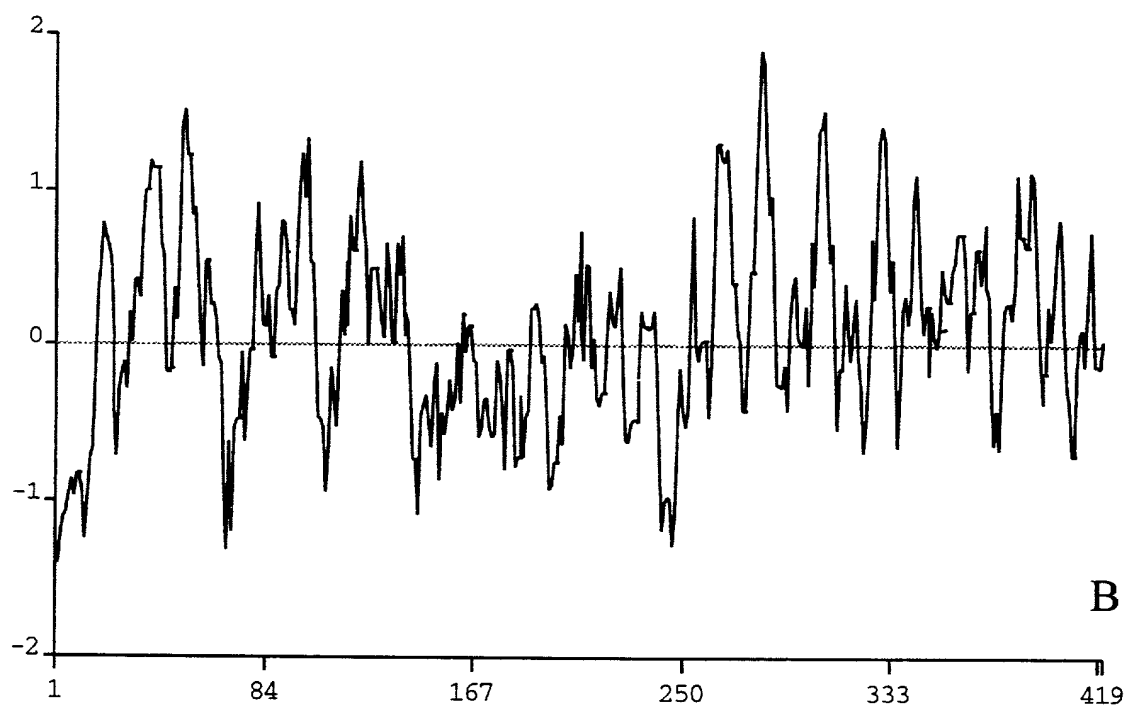
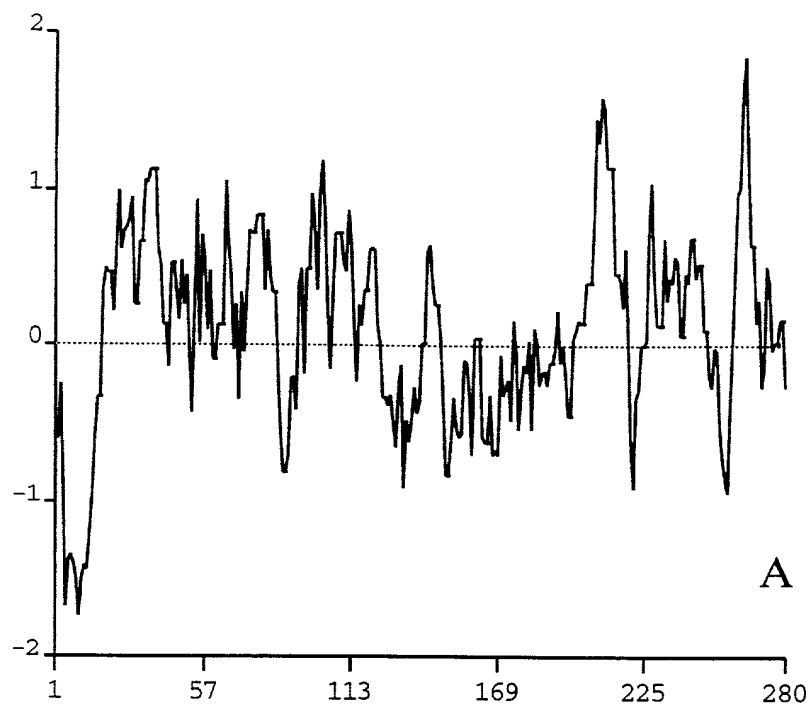


FIGURE 3